
 WIRE (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MSrch_pp protein - protein database search, using Smith-Waterman algorithm
 on: Wed Aug 20 09:54:07 1997; MasPar time 12.22 Seconds
 659.595 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-469-637A-2
 Description: (22-401) from US08469637A.pep (2 of 2)
 Perfect Score: 2861
 Sequence: 1 ETFFPKYLYHDETSHQLLC.....OKLFLENIGNQVOSVKISCL 380

Scoring table: PAM 150
 Gap 11

Searched: 59021 segs, 21210388 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot34
 1:part1 2:part2 3:part3 4:part4 5:parts 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11

Statistics: Mean 48.034; Variance 81.732; scale 0.588
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

ult	No.	Score	Query Match	Length	ID	Description	Pred. No.
1	405	14.2	461	9	TNR2_HUMAN	TUMOR NECROSIS FACTOR	6.30e-63
2	375	13.1	474	9	TNR2_MOUSE	TUMOR NECROSIS FACTOR	5.56e-56
3	303	10.6	277	2	CD40_HUMAN	CD40L RECEPTOR PRECUR	2.64e-40
4	294	10.3	289	2	CD40_MOUSE	CD40L RECEPTOR PRECUR	2.31e-38
5	269	9.4	326	10	VT2_MYVL	LYMPHOTOXIN-BETA RECE	5.03e-33
6	265	9.3	415	9	TNR2_MOUSE	TUMOR NECROSIS FACTOR	3.52e-32
7	260	9.1	325	10	VT2_SFVKA	LYMPHOTOXIN-BETA RECE	3.98e-31
8	260	9.1	435	9	TNR2_MOUSE	TUMOR NECROSIS FACTOR	3.98e-31
9	230	8.0	349	10	VC22_VARY	LYMPHOTOXIN-BETA RECE	6.59e-25
10	221	7.7	454	9	TNR1_MOUSE	TUMOR NECROSIS FACTOR	4.45e-23
11	220	7.7	461	9	TNR1_RAT	TUMOR NECROSIS FACTOR	7.09e-22
12	215	7.5	416	6	NGFR_CHICK	LOW-AFFINITY NERVE GR	7.20e-22
13	213	7.4	427	6	NGFR_HUMAN	LOW-AFFINITY NERVE GR	1.81e-21
14	207	7.2	425	6	NGFR_RAT	LOW-AFFINITY NERVE GR	2.85e-20
15	188	6.6	323	3	FASL_BOVIN	FASL RECEPTOR PRECURS	1.51e-16
16	186	6.5	461	9	TNR1_PIG	TUMOR NECROSIS FACTOR	3.67e-16
17	178	6.2	595	9	CD30_HUMAN	CD30L RECEPTOR PRECUR	1.24e-14
18	172	6.0	455	9	TNR1_HUMAN	TUMOR NECROSIS FACTOR	1.67e-13
19	159	5.6	256	1	41BB_MOUSE	4-1BB LIGAND RECEPTOR	4.22e-11
20	159	5.6	260	2	CD27_HUMAN	CD27L RECEPTOR PRECUR	4.22e-11
21	146	5.1	231	7	OX40_RAT	OX40L RECEPTOR PRECUR	8.91e-09
22	144	5.0	272	7	OX40_MOUSE	OX40L RECEPTOR PRECUR	2.00e-08

RESULT	1	STANDARD	PRT	461 AA.
ID	TNR2_HUMAN			
AC	P20333			
DT	01-FEB-1991 (REL. 17, CREATED)			
DT	01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)			
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)			
DE	TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR			
DE	BINDING PROTEIN 2) (TBPLI) (P80) (TNF-R2) (P75) (CD120B).			
GN	TNFR2 OR TNFR.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; PRIMATES.			
NP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 90260639.			
RA	SMITH C.A., DAVIS T., ANDERSON D., SOLAM L., BECKMANN M.P., JERZY R.,			
RA	DOWER S.K., COSMAN D., GOODWIN R.G.,			
RL	SCIENCE 248:1019-1023(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 91045991.			
RA	KOHNO T., BREWER M.T., BAKER S.L., SCHWARTZ P.E., KING M.W.,			
RA	HALE K.K., SOUJRES C.H., THOMPSON R.C., VANNICE J.L.,			
RA	PROC. NATL. ACAD. SCI. U.S.A. 87:8331-8335(1990).			
RN	[3]			
RP	SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE: 90349572.			
RA	HELLER R.A., SONG K., ONASCH M.A., FISCHER W.H., CHANG D.,			
RA	RINDOLD G.M.,			
RL	PROC. NATL. ACAD. SCI. U.S.A. 87:6151-6155(1990).			
RN	[4]			
RP	SEQUENCE OF 27-31.			
RX	MEDLINE: 90110215.			
RA	ENGELMANN H., NOVICK D., WALLACH D.,			
RA	J. BIOL. CHEM. 265:1531-1536(1990).			
RN	[5]			
RP	SEQUENCE OF 22-40: 65-69; 136-141; 300-306 AND 346-362.			
RX	MEDLINE: 91056048.			
RA	LOETSCHER H., SCHLAGER E.J., LAHM H.-W., PAN Y.-C.E., LESSLAUER W.,			
RA	BROCKHAUS M.,			
RL	J. BIOL. CHEM. 265:20131-20138(1990).			
RN	[6]			
RP	CHARACTERIZATION.			
RX	MEDLINE: 93016040.			
RA	PENNICK D., LAM V.T., MIZE N.K., WEBER R.F., LEWIS M., FENDLY B.M.,			
RA	LIPART M.T., GOEDDEL D.V.,			

ALIGNMENTS

23	140	4.9	255	1	41BB_HUMAN	4-1BB LIGAND RECEPTOR	9.85e-08
24	141	4.9	277	3	OX40_HUMAN	OX40L RECEPTOR PRECUR	6.62e-08
25	137	4.8	327	7	FASL_MOUSE	FASL RECEPTOR PRECURS	3.22e-07
26	134	4.7	250	2	CD27_MOUSE	CD27L RECEPTOR PRECUR	1.04e-06
27	134	4.7	335	3	FASL_HUMAN	FASL RECEPTOR PRECURS	1.04e-06
28	124	4.3	103	10	VA53_VACCC	PROTEIN A53.	4.67e-05
29	124	4.3	103	10	VA53_VACCC	PROTEIN A53.	4.67e-05
30	115	4.0	360	11	YIH9_YEAST	HYPOTHETICAL 41.6 KD	1.24e-03
31	110	3.8	535	3	D2_DICDI	CAMP-REGULATED D2 PRO	7.20e-03
32	105	3.7	2813	10	VWF_HUMAN	VON WILLEBRAND FACTOR	3.96e-02
33	102	3.6	3084	6	LMAL_MOUSE	LAMININ ALPHA-1 CHAIN	1.07e-01
34	101	3.5	712	4	GFAL_CANAL	GLUCOSAMINE--FRUCTOSE	1.49e-01
35	101	3.5	1122	11	YG3C_YEAST	HYPOTHETICAL 128.8 KD	1.49e-01
36	100	3.5	1152	3	DESP_HUMAN	DESMOPLAKIN 1 AND 11	2.05e-01
37	99	3.5	2670	11	YA05_SCHPO	PUTATIVE TRANSLATIONA	2.83e-01
38	96	3.4	431	7	PHOR_SHIDY	PHOSPHATE REGULON SEN	7.33e-01
39	98	3.4	494	7	PR31_YEAST	PRE-MRNA SPLICING FAC	3.90e-01
40	96	3.4	1104	9	SVY_YEAST	VAIYL-TRNA SYNTHETASE	7.33e-01
41	96	3.4	1203	10	XCP_E_XENLA	CHROMOSOME ASSEMBLY P	7.33e-01
42	96	3.4	1356	5	KAB7_YEAST	PROBABLE SERINE/THREO	7.33e-01
43	98	3.4	1947	6	MYSC_CAEEL	MYOSIN HEAVY CHAIN C	3.90e-01
44	96	3.4	3707	7	PCBM_MOUSE	BASEMENT MEMBRANE-SPE	7.33e-01
45	97	3.4	4092	3	DYHC_YEAST	DYNEIN HEAVY CHAIN, C	5.36e-01

[illegible]

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUKARYOTA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89356608.
 RA STAMENKOVIC I., CLARK E.A., SEED B.;
 RL EMBL J. 8.1403-1410(1989).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: X60592; G29851.
 DR PIR: S04460; S04460.
 DR MIN: 109535; TNFR_NGFR.
 DR PROSITE: PS00652; TNFR_NGFR.
 DR RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 277
 FT DOMAIN 20 193 CD40L RECEPTOR.
 FT TRANSMEM 194 215
 FT DOMAIN 216 277
 FT DOMAIN 25 187 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 25 60 4 X TNFR-CYS.
 FT REPEAT 61 103 TNFR-CYS 1.
 FT REPEAT 104 144 TNFR-CYS 2.
 FT REPEAT 145 187 TNFR-CYS 3.
 FT REPEAT 153 187 TNFR-CYS 4.
 FT CARBOHYD 153 187
 FT CARBOHYD 180 180
 FT SEQUENCE 277 AA; 30619 MW; 38284411 CRC32;
 SQ
 Query Match 10.6%; Score 303; DB 2; Length 277;
 Best Local Similarity 36.8%; Pred. No. 2,64e-40;
 Matches 56; Conservative 21; Mismatches 67; Indels 8; Gaps 7;
 Db 38 cdicpgpgklvdcetefeteciclpesefldtmrrethghkycdpn-1glr-vqgkq 95
 41 CDKCPGGTYLKHCHAKKMTVCAPCPDHYTDSWHTSDEC-L--YCSFVCKELQYVKQEC 97
 Qy 96 tseidltcctceegwhctseacescvlhscspgfygkqatvgsdlcepcpgvffsnvs 155
 98 NRTNHRVCECKEGRY-L-EI-EFCLKHSRCPGFGVQAGTPERNTVCRCRCPDGFSSNET 154
 Db 156 safekchpwtscetkdlvvgqagqtktdvvcg 187
 155 SSKAPCRKHTNCSVFGLLTQKGNATHDNICS 186
 Qy
 U.LT 4
 CD40_MOUSE STANDARD: PRT: 289 AA.
 AC P27512;
 DT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
 GN CD40.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUKARYOTA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92105763.
 RA TORRES R.M., CLARK E.A.;
 RL J. IMMUNOL. 148:620-626(1992).
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: M94129; G192526; JOINED.
 DR EMBL: M94128; G192526; JOINED.
 DR PIR: A46476; A46476.
 DR HSSP: P19438; TNFR.
 DR PROSITE: PS00652; TNFR_NGFR.
 DR RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 289
 FT DOMAIN 20 193 CD40L RECEPTOR.
 FT TRANSMEM 194 215
 FT DOMAIN 216 289
 FT DOMAIN 25 187
 FT REPEAT 25 60 4 X TNFR-CYS.
 FT REPEAT 61 103 TNFR-CYS 1.
 FT REPEAT 104 144 TNFR-CYS 2.
 FT REPEAT 145 187 TNFR-CYS 3.
 FT CARBOHYD 153 187
 FT SEQUENCE 289 AA; 32111 MW; D8D70A2C CRC32;
 SQ
 Query Match 10.3%; Score 294; DB 2; Length 289;
 Best Local Similarity 38.8%; Pred. No. 2,31e-38;
 Matches 59; Conservative 20; Mismatches 65; Indels 8; Gaps 6;
 Db 38 cdicpgsrlshetalktqchpdsgefsaqvirelchqhncepn-qglr-vxkqg 95
 41 CDKCPGGTYLKHCHAKKMTVCAPCPDHYTDSWHTSDEC-LY--CSFVCKELQYVKQEC 97
 Qy 96 taesdtvctckegqchctskdeacaghtpcipgfygmamatetdtvchppvffsnqs 155
 98 NRTNHRVCECKEGRY-L-EI-EFCLKHSRCPGFGVQAGTPERNTVCRCRCPDGFSSNET 154
 Db 156 slfekcympscedknhlevlqgtsqtnvvcg 187
 155 SSKAPCRKHTNCSVFGLLTQKGNATHDNICS 186
 Qy
 RESULT 5
 VT2_MYXVL STANDARD: PRT: 326 AA.
 AC P29825;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
 GN T2.
 OS MYXOMA VIRUS (STRAIN LAUSANNE).
 OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXYVIRIDAE; CHOROPPOXYVIRINAE;
 OC LEPORIPPOXYVIRUSES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91335768.
 RA UPTON C., MACEN J.L., SCHREIBER M., MCFADDEN G.;
 RL VIOLOGY. 184:370-382(1991).
 CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 REACH CELLULAR TARGET AND THEREBY DEAMENING THE POTENTIAL
 ANTI-VIRAL EFFECTS OF THE CYTOKINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: M95181; G332310.
 DR EMBL: A23729; E199442.
 DR PIR: A40566; G0Y2ML.
 DR HSSP: P19438; TNFR.
 DR PROSITE: PS00652; TNFR_NGFR.
 DR RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.
 FT SIGNAL 1 16
 FT CHAIN 17 326
 FT DOMAIN 27 186 4 X TNFR-CYS.

RA HOWARD M., COCKAYNE D.A.;
 RL J. IMMUNOL. 149:3921-3926(1992).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: M8312; G1553059; JOINED.
 DR EMBL: M94126; G192526; JOINED.
 DR EMBL: M94129; G192526; JOINED.
 DR EMBL: M94128; G192526; JOINED.
 DR EMBL: M94127; G192526; JOINED.
 DR PIR: A46476; A46476.
 DR HSSP: P19438; TNFR.
 DR PROSITE: PS00652; TNFR_NGFR.
 DR RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 289
 FT DOMAIN 20 193 CD40L RECEPTOR.
 FT TRANSMEM 194 215
 FT DOMAIN 216 289
 FT DOMAIN 25 187
 FT REPEAT 25 60 4 X TNFR-CYS.
 FT REPEAT 61 103 TNFR-CYS 1.
 FT REPEAT 104 144 TNFR-CYS 2.
 FT REPEAT 145 187 TNFR-CYS 3.
 FT CARBOHYD 153 187
 FT SEQUENCE 289 AA; 32111 MW; D8D70A2C CRC32;
 SQ
 Query Match 10.3%; Score 294; DB 2; Length 289;
 Best Local Similarity 38.8%; Pred. No. 2,31e-38;
 Matches 59; Conservative 20; Mismatches 65; Indels 8; Gaps 6;
 Db 38 cdicpgsrlshetalktqchpdsgefsaqvirelchqhncepn-qglr-vxkqg 95
 41 CDKCPGGTYLKHCHAKKMTVCAPCPDHYTDSWHTSDEC-LY--CSFVCKELQYVKQEC 97
 Qy 96 taesdtvctckegqchctskdeacaghtpcipgfygmamatetdtvchppvffsnqs 155
 98 NRTNHRVCECKEGRY-L-EI-EFCLKHSRCPGFGVQAGTPERNTVCRCRCPDGFSSNET 154
 Db 156 slfekcympscedknhlevlqgtsqtnvvcg 187
 155 SSKAPCRKHTNCSVFGLLTQKGNATHDNICS 186
 Qy
 RESULT 5
 VT2_MYXVL STANDARD: PRT: 326 AA.
 AC P29825;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
 GN T2.
 OS MYXOMA VIRUS (STRAIN LAUSANNE).
 OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXYVIRIDAE; CHOROPPOXYVIRINAE;
 OC LEPORIPPOXYVIRUSES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91335768.
 RA UPTON C., MACEN J.L., SCHREIBER M., MCFADDEN G.;
 RL VIOLOGY. 184:370-382(1991).
 CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 REACH CELLULAR TARGET AND THEREBY DEAMENING THE POTENTIAL
 ANTI-VIRAL EFFECTS OF THE CYTOKINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: M95181; G332310.
 DR EMBL: A23729; E199442.
 DR PIR: A40566; G0Y2ML.
 DR HSSP: P19438; TNFR.
 DR PROSITE: PS00652; TNFR_NGFR.
 DR RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.
 FT SIGNAL 1 16
 FT CHAIN 17 326
 FT DOMAIN 27 186 4 X TNFR-CYS.

	DISULFID	104	124	BY SIMILARITY.
FT	DISULFID	126	132	BY SIMILARITY.
FT	DISULFID	139	150	BY SIMILARITY.
FT	DISULFID	142	169	BY SIMILARITY.
FT	DISULFID	172	187	BY SIMILARITY.
FT	CARBOHYD	40	40	POTENTIAL.
FT	CARBOHYD	179	179	POTENTIAL.
SO	SEQUENCE	415 AA;	44956 MM;	3C5DD121 CRC32;
Query Match				
	Best Local Similarity	28.9%;	Score 265;	DB 9;
	Matches	54;	Conservative	30;
			Pred. No. 3,52e-32;	Length 415;
			Mismatches 92;	Indels 11;
			Gaps	8
Db	52 epmhddccscrcpbggefafavcsrsqdtvckctcphmsnnehmhlstcdlcrp-cdiylgf	110		
QY	34 ETSHQLCDCKCPGTLYLKQCHTAKMKVCAPCPDHYTDSMHTSDCLYCSPVCKE-LQY	92		
Db	111 eevapcsdskraecrcpghmscgvllidncchceeerlvgcpgraeavteimdtvncv	170		
QY	93 VK-QECNRTHNRVCEKEGR---YLETE--FCLKNR-S-CPPEGV-VQAGTPERRNVCK	143		
Db	171 pckpghfqnscspracqphltceigglveaapqtsydtcknppegamllailsl	230		
QY	144 RCPGFEFSNESSNAKPRKHTNCSVFELLTLQKGNARHNDNIGSNSSTQKCGIDVLTCE	203		
Db	231 vllfltf	237		
QY	204 EAEFRFA	210		
RESULT 7				
ID	VT2_SEVKA	STANDARD;	PRT;	325 AA.
AC	P25943;			
DT	01-MAY-1992 (REL. 22, CREATED)			
DT	01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)			
DE	01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)			
DE	TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).			
GN	T2.			
OS	SHOPE FIBROMA VIRUS (STRAIN KASZA) (SFV).			
OC	VARIDAE; DS-DNA ENVELOPED VIRUSES; POXYIRIDAE; CHORDOPOXVIRINAE;			
OC	LEPORIPOVIRUSES.			
RN	[1]			
RX	SEQUENCE FROM N.A.			
RX	MEDLINE; 87321103.			
RA	UPTON C., DELANGE A.M., MCFADDEN G.;			
RA	UPTON C., DELANGE A.M., MCFADDEN G.;			
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 176:335-342(1991).			
CC	-1- FUNCTION. BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO			
CC	REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL			
CC	ANTIVIRAL EFFECTS OF THE CYTOKINE.			
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
DR	EMBL; M17433; -. NOT ANNOTATED_CDS.			
DR	EMBL; A23727; E199408; -.			
DR	PIR; B43692; B43692.			
DR	HSSP; P19438; 1TNR.			
KW	PROSITE; PS00652; TNFR-NGFR.			
FT	RECEPTOR. GLYCOPROTEIN. REPEAT; SIGNAL.			
FT	SIGNAL	1	16	POTENTIAL.
FT	CHAIN	17	325	POTENTIAL.
FT	DOMAIN	27	186	PROTEIN T2.
FT	REPEAT	27	62	4 X TNFR-CYS.
FT	REPEAT	27	62	TNFR-CYS 1.
FT	REPEAT	63	104	TNFR-CYS 2.
FT	REPEAT	105	147	TNFR-CYS 3.
FT	REPEAT	148	186	TNFR-CYS 4.
FT	CARBOHYD	105	105	POTENTIAL.
FT	CARBOHYD	181	181	POTENTIAL.
FT	CARBOHYD	205	205	POTENTIAL.
FT	CARBOHYD	238	238	POTENTIAL.


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FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 191 BY SIMILARITY.
FT DISULFID 185 195 BY SIMILARITY.
FT CARBOHYD 54 54 POTENTIAL.
FT CARBOHYD 151 151 POTENTIAL.
FT CARBOHYD 201 201 POTENTIAL.
SO SEQUENCE 461 AA: 50969 MW; 82F68B08 CRC32;

Query Match
Best Local Similarity 33.8%; Score 220; DB 9; Length 461;
Matches 49; Conservative 22; Mismatches 63; Indels 11; Gaps 10;

Db
49 yabpknslcckckhkytlvsdcpspggetvcvcdkgtffasqnhvrgclsktcrke 108
1 YEELSHOLCKCPGTYLKHCHTAK-WKTVCAPCPDHYTDSMTSDECLYCSPVCKE 89
109 mfgvetspckadmdvcgckknqfgrlysethfgvcvdcspcfng-tvtipckekqntvcn 167
90 L-QYVKQECNRRHNRVCECK--E-GRYL-EIEF-CLKHRSCEPGFGVQAGTPERNTVCK 143
168 -chagfflsgnecpsckknqec 191
144 RCPDGF-S-NETSSKAPCKHTNC 166

OY
12 NGFR-CHICK STANDARD: PRT: 416 AA.
ID NGFR-CHICK STANDARD: PRT: 416 AA.
AC P18519;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE (GP80-LNGFR).
DE GALLUS GALLUS (CHICKEN).
DE EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC GALLIFORMES.
OC [1]
OC SEQUENCE FROM N.A.
OC TISSUE-BRAIN:
RC MEDLINE: 9016579.
RX LARKE T.H., WESKAMP G., HEIDER J.C., RADEKE M.J., MISKO T.P.,
RA SHOOTER E.M., REICHARDT L.F.;
RA NEURON 2:1123-1134(1989).
[2]
RA SEQUENCE OF 21-416 FROM N.A.
RA MEDLINE: 90152140.
RA HEIDER J.G., FATEMIE-NAINE S., WHEELER E.F., BOTHWELL M.;
RL DEV. BIOL. 137:287-304(1990).
CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
CC NT-3, AND NT-4.
CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
CC BOND FORMATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR PIR: J00006; J00006.
DR PIR: A60504; A60504.
DR PROSITE: PS00652; TNFR_NGFR.
DR RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
KW PHOSPHORYLATION; SIGNAL.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 416 NGF RECEPTOR.
FT DOMAIN 29 239 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 240 261 POTENTIAL.
FT DOMAIN 262 416 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 181 4 X TNFR-CYS.
FT REPEAT 23 57 TNFR-CYS 1.
FT REPEAT 58 100 TNFR-CYS 2.

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FT REPEAT 101 140 TNFR-CYS 3.
FT REPEAT 141 181 TNFR-CYS 4.
FT DOMAIN 188 236 SER/THR-RICH.
FT DOMAIN 333 410 DEATH DOMAIN.
FT DISULFID 24 35 BY SIMILARITY.
FT DISULFID 36 49 BY SIMILARITY.
FT DISULFID 39 56 BY SIMILARITY.
FT DISULFID 59 75 BY SIMILARITY.
FT DISULFID 78 91 BY SIMILARITY.
FT DISULFID 81 99 BY SIMILARITY.
FT DISULFID 101 114 BY SIMILARITY.
FT DISULFID 117 130 BY SIMILARITY.
FT DISULFID 120 138 BY SIMILARITY.
FT DISULFID 141 156 BY SIMILARITY.
FT DISULFID 159 172 BY SIMILARITY.
FT DISULFID 162 180 BY SIMILARITY.
FT CARBOHYD 52 52 POTENTIAL.
FT CONFLICT 36 36 C->Y (IN REF. 2).
FT CONFLICT 173 173 T->K (IN REF. 2).
FT CONFLICT 276 276 N->S (IN REF. 2).
FT CONFLICT 396 396 K->R (IN REF. 2).
SO SEQUENCE 416 AA: 44654 MW; 4D3F086A CRC32;

Query Match
Best Local Similarity 30.4%; Score 215; DB 6; Length 416;
Matches 45; Conservative 27; Mismatches 70; Indels 6; Gaps 6;

Db
36 ckacnlsggvvqpcgvn-qtvcepeldsvtsdvsatepckpctq-cvghlmsapcve 93
41 CDKCPGTYLKHCHTAKKTVCAPCPDHY-YTDSWHTSDECLYCSPVCKELQYVKQECNR 99
94 sddavcraygyfddelsgscckscicevgfqlmfcordsdvcecpgeglfsdeanf 153
100 TNHRCCECKEGRYL-EIE-FCLKHRSCEPGFGVQAGTPERNTVCKRCPDGFSSNETSSK 157
154 dpcldpcticeenwvke-ctatsdaec 180
158 APCRKHTNCVSFGLLTOKGNATHDNC 185

OY
13 NGFR-HUMAN STANDARD: PRT: 427 AA.
ID NGFR-HUMAN STANDARD: PRT: 427 AA.
AC P08138;
DT 01-AUG-1988 (REL. 08, CREATED)
DT 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE (GP80-LNGFR).
DE GN NGFR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUHERIA; PRIMATES.
OC [1]
OC SEQUENCE FROM N.A.
OC MEDLINE: 87051725.
RX JOHNSON D., LANAHAN A., BUCK C.R., SEHGAL A., MORGAN C., MERCER E.,
RA BOTHWELL M., CHAO M.;
RL CELL 47:545-554(1986).
CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
CC NT-3, AND NT-4.
CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
CC BOND FORMATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: M14764; G189205; -.
DR PIR: A25218; G0HUN.
DR HSSP: P19438; TNFR.
DR MIM: 162010; -.
DR PROSITE: PS00652; TNFR_NGFR.
DR RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
KW PHOSPHORYLATION; SIGNAL.

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FT SIGNAL 1 28
FT CHAIN 29 427
FT DOMAIN 29 250
FT TRANSMEM 251 272
FT DOMAIN 273 427
FT DOMAIN 31 189
FT REPEAT 31 65
FT REPEAT 66 107
FT REPEAT 108 147
FT REPEAT 148 189
FT REPEAT 189 250
FT DOMAIN 344 421
FT DISULFID 32 43
FT DISULFID 44 57
FT DISULFID 47 64
FT DISULFID 67 83
FT DISULFID 86 99
FT DISULFID 89 107
FT DISULFID 109 122
FT DISULFID 125 138
FT DISULFID 128 146
FT DISULFID 149 164
FT DISULFID 167 180
FT DISULFID 170 188
FT DOMAIN 197 248
FT CARBOHYD 60 60
SQ SEQUENCE 427 AA: 45183 MW: EE2924BD CRC32:

Query Match 7.48; Score 213; DB 6; Length 427;
Best Local Similarity 34.9%; Pred. No. 1.81e-21;
Matches 45; Conservative 19; Mismatches 60; Indels 5; Gaps 5;

Db 44 ckacnlgevgagpcgan-qvcepcldsvfsvdvsatepckpcte-cvqlgmsapcve 101
OY 41 CDKCPRGTYLKHCHTAKMKVCAPCPDHY-YTDSWHTSDCLYCSPVCKELQVQKQECNR 99
Db 102 addavrcceaygygdeetgycceacrcvceagsglvfscqdknvtvcecpdgtylsdeanhv 161
OY 100 THNRVCECKEGRL-EL-EKCLKHSRCPFGVQAGTPERNVCKRCRCPDGFSSNETSSK 157
Db 162 dpcldpctvc 170
OY 158 APCRKHTNC 166

RESULT 14
ID NGFR_RAT STANDARD: PRT: 425 AA.
AC P07174;
AC 01-APR-1988 (REL. 07, CREATED)
RA 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
RL 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
RN NATURE 325:593-597(1987).
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE (GP80-LNGFR).
GN NGFR.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE: 87115859.
RA RADEKE M.J., MISKO T.P., HSU C., HERZENBERG L.A., SHOOTER E.M.;
RL NATURE 325:593-597(1987).
RN [2]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE-LIVER;
RX MEDLINE: 93077038.
RA METSIS M., TIMUSK T., ALLIKMETS R., SAARMA M., PERSSON H.;
RL GENE 121:247-254(1992).
RN [1]
RP FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
CC NT-3, AND NT-4.
CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
CC -1- BOND FORMATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.

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CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: X05137; G56756; -.
DR EMBL: X61269; -. NOT_ANNOTATED_CDS.
DR PIR: A26431; A26431.
DR HSSP: P19438; 1TNR.
DR PROSITE: PS00652; TNFR_NGFR.
DR PROSITE: PS50017; DEATH_DOMAIN.
DR RECEPTOR: NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
KW PHOSPHORYLATION; SIGNAL.
FT SIGNAL 1 29
FT CHAIN 30 425
FT DOMAIN 30 251
FT TRANSMEM 252 273
FT DOMAIN 274 425
FT DOMAIN 32 190
FT REPEAT 32 66
FT REPEAT 67 108
FT REPEAT 109 148
FT REPEAT 149 190
FT REPEAT 198 249
FT DOMAIN 354 419
FT DISULFID 33 44
FT DISULFID 45 58
FT DISULFID 48 65
FT DISULFID 68 84
FT DISULFID 87 100
FT DISULFID 90 108
FT DISULFID 110 123
FT DISULFID 126 139
FT DISULFID 129 147
FT DISULFID 150 165
FT DISULFID 168 181
FT DISULFID 171 189
FT CARBOHYD 61 61
SQ SEQUENCE 425 AA: 45432 MW: 7D78F258 CRC32:

Query Match 7.28; Score 207; DB 6; Length 425;
Best Local Similarity 33.3%; Pred. No. 2.85e-20;
Matches 43; Conservative 21; Mismatches 60; Indels 5; Gaps 4;

Db 45 ckacnlgevgagpcgan-qvcepcldsvfsvdvsatepckpcte-clglsmsapcve 102
OY 41 CDKCPRGTYLKHCHTAKMKVCAPCPDHY-YTDSWHTSDCLYCSPVCKELQVQKQECNR 99
Db 103 addavrcceaygygdeetgycceacrcvceagsglvfscqdknvtvcecpdgtylsdeanhv 162
OY 100 THNRVCECKEGRL-EL-EKCLKHSRCPFGVQAGTPERNVCKRCRCPDGFSSNETSSK 157
Db 163 dpcldpctvc 171
OY 158 APCRKHTNC 166

RESULT 15
ID FAS_A BOVIN STANDARD: PRT: 323 AA.
AC P51867;
AC 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95).
GN APT1 OR FAS.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96226401.
RA YOO J., STONE R.T., BEATTIE C.W.;
RL DNA CELL BIOL. 15:227-234(1996).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. MEDIATES
CC CELL DEATH. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE

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CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: U34794; G1262193; -.
KW APOPTOSIS; RECEPTOR; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 323 FAST RECEPTOR.
FT DOMAIN 17 170 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 171 168 POTENTIAL.
FT DOMAIN 189 323 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 45 163 3 X TNFR-CYS.
FT REPEAT 45 80 TNFR-CYS 1.
FT REPEAT 81 124 TNFR-CYS 2.
FT REPEAT 125 163 TNFR-CYS 3.
FT DOMAIN 222 302 DEATH DOMAIN.
SQ SEQUENCE 323 AA: 36445 MW: 36445 CRC32;

Query Match 6.68; Score 188; DB 3; Length 323;
Best Local Similarity 35.78; Pred. NO. 1.51e-16;
Matches 40; Conservative 17; Mismatches 49; Indels 6; Gaps 6;
Db 53 hgfcgpcppgkxngdcxrdgdtpevcylseegneytdkshsdcklrcs-1cdeehgle 111
OY 37 HOLLCDKCPGPTYLKQHCITAKMKTV-CAPCPD-HYTDSWHTSDECLYCSPVCKELQ-Y- 92
Db 112 vegnctrlntkrcrkcnfscnsspcchncpctcehngliekctpsantkck 163
OY 93 VKQECNRTNHRVCECKEGRYLEIEFLKHSRCPG-GFGVYQAGTPERNTVCK 143

Search completed: Wed Aug 20 09:55:23 1997
Job time : 76 secs.